Applicant: Jennifer Richardson et al. Attorney's Docket No.: 07334-312001

Serial No.: 09/967,305

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Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

<u>Listing of Claims</u>:

1-32. (Canceled).

- 33. (Currently amended) A method for identifying candidate therapeutic agents for the treatment of prostate cancer, the method comprising:
- (a) obtaining a test sample comprising prostate tumor cells encoding a protein having the amino acid sequence of SEQ ID NO:2;
 - (b) exposing the test sample to a test compound;
- (c) measuring the level of expression of alpha-methylacyl-CoA racemase mRNA comprising the nucleotide sequence of SEQ ID NO:3 wherein a U is substituted for each T in the test sample exposed to the test compound; and
- (d) identifying the test compound as a candidate therapeutic agent for the treatment of prostate cancer if the level of expression of alpha-methylacyl-CoA racemase mRNA in the test sample exposed to the test compound is less than in a control test sample not exposed to the test compound.
- 34. (Previously presented) The method of claim 33 wherein step (c) comprises exposing the test sample to a nucleic acid probe which hybridizes to a nucleic acid molecule consisting of SEQ ID NO:3 under hybridization in 0.5M sodium phosphate, 7% SDS at 65°C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C, wherein the nucleic acid probe comprises a fragment of the full-length complement of SEQ ID NO:3.

35-58. (Canceled).

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59. (Previously presented) The method of claim 34 wherein step (c) comprises contacting alpha-methylacyl-CoA racemase mRNA with a nucleic acid probe comprising a fragment of the full-length complement of SEQ ID NO:3 the fragment comprising at least 15 consecutive nucleotides of the full-length complement of SEQ ID NO:3.

- 60. (Previously presented) The method of claim 59 wherein the probe comprises at least 20 consecutive nucleotides of the full-length complement of SEQ ID NO:3.
- 61. (Previously presented) The method of claim 59 wherein the probe comprises at least 25 consecutive nucleotides of the full-length complement of SEQ ID NO:3.
- 62. (Previously presented) The method of claim 59 wherein the probe comprises at least 30 consecutive nucleotides of the full-length complement of SEQ ID NO:3.
- 63. (Previously presented) The method of claim 59 wherein the probe comprises at least 40 consecutive nucleotides of the full-length complement of SEQ ID NO:3.
- 64. (Previously presented) The method of claim 59 wherein the probe comprises at least 50 consecutive nucleotides of the complement of SEQ ID NO:3.
- 65. (Previously presented) The method of claim 59 wherein the probe comprises at least 75 consecutive nucleotides of the full-length complement of SEQ ID NO:3.
- 66. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 260 nucleotides.
- 67. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 300 nucleotides.

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68. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 400 nucleotides.

- 69. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 500 nucleotides.
- 70. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 800 nucleotides.
- 71. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 900 nucleotides.
- 72. (Currently amended) The method of claim 34 wherein the nucleic acid probe comprises at least [900] 1000 nucleotides.
- 73. (Previously presented) The method of claim 59 wherein the probe is immobilized on a surface.
- 74. (Previously presented) The method of claim 34 wherein the alpha-methylacyl-CoA racemase mRNA is immobilized on a surface.
- 75. (Previously presented) The method of claim 33 wherein step (c) comprises amplification of the alpha-methylacyl-CoA racemase mRNA.
- 76. (Previously presented) The method of claim 59 wherein the probe is detectably labeled.

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77. (Previously presented) The method of claim 76 wherein the detectable label is selected from the group consisting of a chemiluminescent label, a fluorescent label, a radioactive label, or a colorimetric label.

- 78. (Previously presented) The method of claim 34 wherein the probe is detectably labeled.
- 79. (Previously presented) The method of claim 78 wherein the detectable label is selected from the group consisting of a chemiluminescent label, a fluorescent label, a radioactive label, or a colorimetric label.